

# SEQUENCE LISTING

<110> Shaughnessy, John D.  
 <120> Evi27 Gene Sequence and Protein Encoded Thereby  
 <130> D6138  
 <140>  
 <141> 2001-02-02  
 <150> US 60/180,374  
 <151> 2000-02-04  
 <160> 9  
 <210> 1  
 <211> 1827  
 <212> DNA  
 <213> *Homo sapiens*  
 <220>  
 <221> prim\_transcript  
 <223> cDNA of human Evi27

<400> 1  
 cggcgatgtc gctcgtgctg ataagcctgg ccgcgctgtg caggagcgc 50  
 gtaccccgag agccgaccgt tcaatgtggc tctgaaactg ggccatctcc 100  
 agagtggatg ctacaacatg atctaattccc cggagacttg agggacctcc 150  
 gagtagaacc tgttacaact agtggtgcaa caggggacta ttcaattttg 200  
 atgaatgtaa gctgggtact ccgggcagat gccagcatcc gcttggtgaa 250  
 ggccaccaag atttgtgtga cgggcaaaag caacttccag tcctacagct 300  
 gtgtgaggtg caattacaca gaggccttcc agactcagac cagaccctct 350  
 ggtggtaaat ggacattttc ctatatcggc ttccctgtag agctgaacac 400  
 agtctatttc attggggccc ataatatcc taatgcaa atgaatgaag 450  
 atggcccttc catgtctgtg aatttcacct caccaggctg cctagaccac 500  
 ataatgaaat ataaaaaaaa gtgtgtcaag gccggaagcc tgtgggatcc 550  
 gaacatcact gcttgtaaga agaattgagga gacagtagaa gtgaacttca 600  
 caaccactcc cctgggaaac agatacatgg ctcttatcca acacagcact 650  
 atcatcgggt tttctcaggt gtttgagcca caccagaaga aacaaacgcg 700  
 agcttcagtg gtgattccag tgactgggga tagtgaagg gctacggtgc 750  
 agctgactcc atattttcct acttggtgga gcgactgcat ccgacataaa 800  
 ggaacagttg tgctctgccc acaaacaggc gtccctttcc ctctggataa 850  
 caacaaaagc aagccgggag gctggctgcc tctcctcctg ctgtctctgc 900  
 tgggtggccac atgggtgctg gtggcaggga tctatcta atgtggaggcac 950  
 gaaaggatca agaagacttc cttttctacc accacactac tgccccccat 1000  
 taaggttctt gtggtttacc catctgaaat atgtttccat cacacaattt 1050  
 gttacttcac tgaatttctt caaaaccatt gcagaagtga ggtcatcctt 1100  
 gaaaagtggc agaaaaagaa aatagcagag atgggtccag tgcagtggct 1150  
 tgccactcaa agaaggcgag cagacaaagt cgtcttcctt ctttccaatg 1200  
 acgtcaacag tgtgtgcat ggtacctgtg gcaagagcga gggcagtcct 1250  
 agtgagaact ctcaagacct cttccccctt gcctttaacc ttttctgcag 1300  
 tgatctaaga agccagattc atctgcacaa atacgtggtg gtctacttta 1350

gagagattga	tacaaaagac	gattacaatg	ctctcagtgt	ctgccccaa	1400
taccacttca	tgaaggatgc	cactgctttc	tgtgcagaac	ttctccatgt	1450
caagcagcag	gtgtcagcag	gaaaaagatc	acaagcctgc	cacgatggct	1500
gctgctcctt	gtagcccacc	catgagaagc	aagagacctt	aaaggcttcc	1550
tatcccacca	attacaggga	aaaaacgtgt	gatgatcctg	aagcttacta	1600
tgcagcctac	aaacagcctt	agtaattaaa	acattttata	ccaataaaa	1650
tttcaaatat	tactaactaa	tgtagcatta	actaacgatt	ggaaactaca	1700
tttacaactt	caaagctgtt	ttatacatag	aatcaatta	cagctttaat	1750
tgaaaactgt	aaccattttg	ataatgcaac	aataaagcat	cttccaaaa	1800
aaaaaaaaaa	aaaaaaaaaa	aaaaaaa			1827

<210> 2  
 <211> 2856  
 <212> DNA  
 <213> *Homo sapiens*

<220>

<221> prim\_transcript  
 <223> cDNA of human Evi27

<400>	2				
cggcgatgtc	gctcgtgctg	ataagcctgg	ccgcgctgtg	caggagcgcc	50
gtaccccgag	agccgaccgt	tcaatgtggc	tctgaaactg	ggccatctcc	100
agagtggatg	ctacaacatg	atctaattccc	cggagacttg	agggacctcc	150
gagtagaacc	tgttacaact	agtgttgcaa	caggggacta	ttcaattttg	200
atgaatgtaa	gctgggtact	ccgggcagat	gccagcatcc	gcttgttgaa	250
ggccaccaag	atgtgtgtga	cgggcaaaaag	caacttccag	tcctacagct	300
gtgtgaggtg	caattacaca	gaggccttcc	agactcagac	cagaccctct	350
ggtggtaaat	ggacattttc	ctatatcggc	ttccctgtag	agctgaacac	400
agtctatttc	attggggccc	ataatattcc	taatgcaa	atgaatgaag	450
atggcccttc	catgtctgtg	aattttcacct	caccaggctg	cctagaccac	500
ataatgaaat	ataaaaaaaa	gtgtgtcaag	gccggaagcc	tgtgggatcc	550
gaacatcact	gcttgtaaga	agaatgagga	gacagtagaa	gtgaacttca	600
caaccactcc	cctgggaaac	agatacatgg	ctcttatcca	acacagcact	650
atcatcggtg	tttctcaggt	gtttgagcca	caccagaaga	aacaaacgcg	700
agcttcagtg	gtgattccag	tgactgggga	tagtgaaggt	gctacggtgc	750
aggtaaagtt	cagtgaagctg	ctctggggag	ggaagggaca	tagaagactg	800
ttccatcatt	cattgctttt	aaggatgagt	tctctcttgt	caaatgcact	850
tctgccagca	gacaccagtt	aagtggcggt	catgggggtt	ctttcgctgc	900
agcctccacc	gtgctgaggt	caggaggccg	acgtggcagt	tgtggtccct	950
tttgcttgta	ttaatggctg	ctgaccttcc	aaagcacttt	ttattttcat	1000
tttctgtcac	agacactcag	ggatagcagt	accattttac	ttccgcaagc	1050
ctttaactgc	aagatgaagc	tgcaaagggt	ttgaaatggg	aagggtttgag	1100
ttccaggcag	cgtatgaact	ctggagaggg	gctgccagtc	ctctctgggc	1150
cgcagcggac	ccagctggaa	cacaggaagt	tggagcagta	ggtgctcctt	1200
cacctctcag	tatgtctctt	tcaactctag	tttttgaagt	ggggacacag	1250
gaagtccagt	ggggacacag	ccactcccca	agaataagg	aacttccatg	1300
cttcattccc	tggcataaaa	agtntcaaaa	cacaccagag	ggggcaggca	1350
ccagccaggg	tatgatgggt	actacccttt	tctggagaac	catagacttc	1400
ccttactaca	gggacttgca	tgtcctaaag	cactggctga	aggaagccaa	1450
gaggatcact	gctgctcctt	ttttgtagag	gaaatgtttg	tgtacgtggt	1500

```

aagatatgac ctagcccttt taggtaagcg aactgggatg ttagtaacgt 1550
gtacaaagtt taggttcaga ccccgaggag cttgggcatg tgggtctcgg 1600
gtcactgggt ttgacttttag ggctttgtta cagatgtgtg accaagggga 1650
aaatgtgcat gacaacacta gaggtagggg cgaagccaga aagaagggaa 1700
gttttggtcg aagtaggagt cttggtgaga ttttgctgtg atgcatgggt 1750
tgaactttct gagcctcttg tttttcctca gctgactcca tattttccta 1800
cttgtggcag cgactgcata cgacataaag gaacagttgt gctctgcca 1850
caaacaggcg tccctttccc tctggataac aacaaaagca agccgggagg 1900
ctggctgcct ctctctctgc tgtctctgct ggtggccaca tgggtgctgg 1950
tggcagggat ctatctaata tggaggcacg aaaggatcaa gaagacttcc 2000
ttttctacca ccacactact gccccccatt aaggttcttg tggtttacc 2050
atctgaaata tgtttccatc acacaatttg ttacttctact gaatttcttc 2100
aaaaccattg cagaagttag gtcatacctt aaaagtggca gaaaaagaaa 2150
atagcagaga tgggtccagt gcagtggctt gccactcaa agaaggcagc 2200
agacaaagtc gtcttccttc tttccaatga cgtcaacagt gtgtgcatg 2250
gtacctgtgg caagagcgag ggcagtccca gtgagaactc tcaagacctc 2300
ttcccccttg cttttaacct tttctgcagt gatctaagaa gccagattca 2350
tctgcacaaa tacgtgggtg tctacttttag agagattgat acaaaagacg 2400
attacaatgc tctcagtgtc tgccccaagt accacttcat gaaggatgcc 2450
actgctttct gtgcagaact tctccatgtc aagcagcagg tgtcagcagg 2500
aaaaagatca caagcctgcc acgatggctg ctgctccttg tagcccaccc 2550
atgagaagca agagacctta aaggcttcct atcccaccaa ttacagggaa 2600
aaaacgtgtg atgatacctga agcttactat gcagcctaca aacagcctta 2650
gtaattaaaa cattttatac caataaaaatt ttcaaataat actaactaat 2700
gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 2750
tatacataga aatcaattac agctttaatt gaaaactgta accattttga 2800
taatgcaaca ataaagcatc ttccaaaaaa aaaaaaaaaa aaaaaaaaaa 2850
aaaaaa

```

```

<210>      3
<211>    1963
<212>      DNA
<213>    Unknown

```

<220>

```

<221>      prim_transcript
<223>      cDNA of mouse Evi27

```

<400> 3

```

gtggccagtg gccgggccat gttgctagtg ttgctgatct tggctgcata 50
gtgcaggagc gccctgcctc gagagccgac tattcagtgt ggctctgaga 100
cagggccatc tccagagtgg atggtccaac acacactcac tccaggagac 150
ttgagggacc tccaagtgga actcgtcaag acaagtgtgg cagcagagga 200
gtttttcaatt ttgatgaaca taagctggat actccgggca gacgccagca 250
tccgcttggt gaaggccacc aagatctgcg tgagtggcaa aaacaacatg 300
aattcataca gctgtgtgag gtgcaactac acagaggcct tccaaagcca 350
gaccagacct tccggcggca aatggacatt ctcttatgta ggcttccctg 400
tggagctgag cactctctat ctcatcagcg ccataacat ccccaatgct 450
aatatgaatg aggacagccc ttctttgtct gtgaacttca cctcgccagg 500
ctgcctaaac cacgtaatga aatataaaaa gcagtgcact gaggcgggaa 550
gcctgtggga cccagacatc actgcttgta aaaagaacga gaagatgggt 600

```

gaagtgaatt	tcacaaccaa	tccccttgga	aacagatata	cgatttctcat	650
tcaacgggac	acgacattgg	ggttttctag	agtgctggag	aataaactga	700
tgaggacgtc	tgtagccatc	ccggtgactg	aggagagtga	aggtgcggtg	750
gttcagctga	ccccatattt	acatacctgc	ggcaatgact	gcattccgacg	800
cgaagggaca	gttgtgcttt	gctcagagac	aagtgtctcc	atccctccag	850
atgacaacag	acgcatgctg	ggaggctggc	tgcctctctt	cctgggtgctg	900
ctgggtggctg	tgtgggtgct	ggcagctggg	atctacctaa	cttggaggca	950
aggaaggagc	acgaagacgt	ccttttcctat	ttccaccatg	ctcctgcccc	1000
tcattaaggt	cctgggtggtt	tatccttctg	agatatgttt	ccatcacacc	1050
gtctgtcgtc	tactgactt	tcttcaaaac	tactgcagaa	gtgagggtcat	1100
ccttgaaaaa	tggcagaaaa	agaaaatcgc	cgagatgggg	ccggtacagt	1150
ggctgaccac	tcagaagcaa	gcggcagata	aagtgggtctt	ccttcttccc	1200
agtgcgtcc	cgaccctttg	tgacagtgcc	tgtggccaca	atgagggcag	1250
cgccagggag	aactctcagg	atctgttccc	tcttgccctt	aacctctttt	1300
gtagtgattt	cagcagccag	acgcattctgc	acaaatacct	ggtggtctat	1350
cttggggggag	cagacctcaa	aggcgactat	aatgcctctga	gtgtctgccc	1400
ccaatatcat	ctcatgaagg	acgccacagc	tttccacaca	gaacttctca	1450
aggctacgca	gagcatgtca	gtgaagaaac	gtcacaagc	ctgccatgat	1500
agctgttcac	ccttgtagtc	caccgggggg	aatagagact	ctgaagcctt	1550
cctactctcc	cttccagtga	caaattgctgt	gtgacgactc	tgaaatgtgt	1600
gggagagggt	gtgtggagggt	agtgtctatgt	acaaacttgc	tttaaaactg	1650
gagtttgcaa	agtcaacctg	agcatacacg	cctgaggcta	gtcattggct	1700
ggatttatga	agacaacaca	gttacagaca	ataatgagtg	ggacctacat	1750
ttgggatata	cccaaagctg	ggtaatgatt	atcactgaga	accacgcact	1800
ctggccatga	agtaatacgg	cacttccctg	tcaggctgtc	tgtcagggttg	1850
ggtctgtctt	gcactgcccc	tgctctatgc	tgcacgtaga	ccgttttgta	1900
acattttta	ctgttaatat	ataatccgtt	tgggaagctc	tcaaaaaaaa	1950
aaaaaaaaa	aaa				1963

<210> 4  
 <211> 2589  
 <212> DNA  
 <213> Unknown

<220>

<221> prim\_transcript  
 <223> cDNA of mouse Evi27

<400> 4

gtggccagtg	gccgggccat	gttgctagtgt	ttgctgatct	tggtctgcac	50
gtgcaggagc	gccctgcctc	gagagccgac	tattcagtgt	ggctctgaga	100
cagggccatc	tccagagtgg	atggtccaac	acacactcac	tccaggagac	150
ttgagggacc	tccaagtgga	actcgtcaag	acaagtgtgg	cagcagagga	200
gttttcaatt	ttgatgaaca	taagctggat	actccgggca	gacgccagca	250
tccgcttggt	gaaggccacc	aagatctgcg	tgagtggcaa	aaacaacatg	300
aattcataca	gctgtgtgag	gtgcaactac	acagaggcct	tccaaagcca	350
gaccagacct	tccggcggca	aatggacatt	ctcctatgta	ggcttccctg	400
tggagctgag	cactctctat	ctcatcagcg	cccataacat	ccccaatgct	450
aatatgaatg	aggacagccc	ttctttgtct	gtgaacttca	cctcgccagg	500
gtgcactcgt	gaaaacacag	aagtaacgtc	cggtgtatgt	ccagcagcta	550
aacaccaggc	tctccggatt	tcagctcctt	tccattaca	atttcctcct	600

```

gggccagagg actcagtcac tctgccaccc cagcctcttg cgctcgctttt 650
tcatgacttt gtcaaactta cctagcttgt ttccattctg aaattgtctg 700
atgcttgctt cgtatgtaag ccggggatat gaggtttggg tatgaatccc 750
acagaggggca ctgaattctt ctactatagg cctatctggg ctgtgtgaca 800
ttgttggtga gggtcgtgcc tactaggcat ctgggtatct accacctgga 850
gcttcatgtc tggaagaggc agaacctata tgtattgtca gctctcactt 900
ttgtttccgt gtcacctcct ggagactggt ttgataaag gttgtactta 950
aaggagatta cttaaagctt ccgtggaaga atggtttcct atttagatct 1000
gttgtctctc atatctgaag taagtgtgtg tgtgtgtgtt ttgtgtgtgt 1050
gtgtgtgtgt gtgtgtgtac tgggcaaagg gttatacctt tactcaaagt 1100
taacaacttt cattcacatt ccagggctgc ctaaaccacg taatgaaata 1150
taaaaagcag tgcactgagg cggaagcct gtgggacca gacatcactg 1200
cttgtaaaaa gaacgagaag atggttgaag tgaatttcac aaccaatccc 1250
cttggaacaa gatacacgat tctcattcaa cgggacacga cattgggggtt 1300
ttctagagtg ctggagaata aactgatgag gacgtctgta gccatcccgg 1350
tgactgagga gagtgaaggc gcggtggttc agctgacccc atatttacat 1400
acctgcggca atgactgcat ccgacgcgaa gggacagttg tgctttgctc 1450
agagacaagt gctcccatcc ctccagatga caacagacgc atgctgggag 1500
gctggctgcc tctcttctct gtgctgctgg tggctgtgtg ggtgctggca 1550
gctgggatct acctaaactg gaggcaagga aggagcacga agacgtcctt 1600
tcctatttcc accatgctcc tgccctcat taaggctctg gtggtttatc 1650
cttctgagat atgtttccat cacaccgtct gtcgcttcac tgactttctt 1700
caaaactact gcagaagtga ggtcatcctt gaaaaatggc agaaaaagaa 1750
aatcgccgag atggggcccg tacagtggct gaccactcag aagcaagcgg 1800
cagataaagt ggtcttctct ctccagtg acgtcccgac cttttgtgac 1850
agtgcctgtg gccacaatga gggcagcgcc agggagaact ctcaggatct 1900
gttccctctt gcctttaacc tctttttag tgatttcagc agccagacgc 1950
atctgcacaa atacctggtg gtctatcttg ggggagcaga cctcaaaggc 2000
gactataatg ccctgagtgt ctgcccccaa tatcatctca tgaaggacgc 2050
cacagctttc cacacagaac ttctcaaggc tacgcagagc atgtcagtga 2100
agaaacgctc acaagcctgc catgatagct gttcaccctt gtagtccacc 2150
cgggggaata gagactctga agccttccta ctctcccttc cagtgacaaa 2200
tgctgtgtga cgactctgaa atgtgtggga gaggtgtgtg ggaggtagtg 2250
ctatgtacaa acttgcttta aaactggagt ttgcaaagtc aacctgagca 2300
tacacgcctg aggctagtca ttggctggat ttatgaagac aacacagtta 2350
cagacaataa tgagtgggac ctacatttgg gatataccca aagctgggta 2400
atgattatca ctgagaacca cgcactctgg ccatgaagta atacggcact 2450
tccctgtcag gctgtctgtc aggttgggtc tgtcttgcac tgcccatgct 2500
ctatgctgca cgtagaccgt tttgtaacat tttaatctgt taatgaataa 2550
tccgtttggg aagctctcaa aaaaaaaaaa aaaaaaaaaa 2589

```

```

<210>      5
<211>      502
<212>      PRT
<213>      Homo sapiens

<220>

<221>      PEPTIDE
<223>      Human Evi27 protein

<400>      5

```

Met	Ser	Leu	Val	Leu	Ile	Ser	Leu	Ala	Ala	Leu	Cys	Arg	Ser	Ala	
				5					10					15	
Val	Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	
				20					25					30	
Ser	Pro	Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	
				35					40					45	
Arg	Asp	Leu	Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	
				50					55					60	
Asp	Tyr	Ser	Ile	Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	
				65					70					75	
Ala	Ser	Ile	Arg	Leu	Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	
				80					85					90	
Lys	Ser	Asn	Phe	Gln	Ser	Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	
				95					100					105	
Glu	Ala	Phe	Gln	Thr	Gln	Thr	Arg	Pro	Ser	Gly	Gly	Lys	Trp	Thr	
				110					115					120	
Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr	Phe	
				125					130					135	
Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly	
				140					145					150	
Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	
				155					160					165	
Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	
				170					175					180	
Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	
				185					190					195	
Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	
				200					205					210	
Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	
				215					220					225	
His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	
				230					235					240	
Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	
				245					250					255	
Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	
				260					265					270	
Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	
				275					280					285	
Lys	Pro	Gly	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val	
				290					295					300	
Ala	Thr	Trp	Val	Leu	Val	Ala	Gly	Ile	Tyr	Leu	Met	Trp	Arg	His	
				305					310					315	
Glu	Arg	Ile	Lys	Lys	Thr	Ser	Phe	Ser	Thr	Thr	Thr	Leu	Leu	Pro	
				320					325					330	
Pro	Ile	Lys	Val	Leu	Val	Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His	
				335					340					345	
His	Thr	Ile	Cys	Tyr	Phe	Thr	Glu	Phe	Leu	Gln	Asn	His	Cys	Arg	
				350					355					360	
Ser	Glu	Val	Ile	Leu	Glu	Lys	Trp	Gln	Lys	Lys	Lys	Ile	Ala	Glu	
				365					370					375	
Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	Thr	Gln	Lys	Lys	Ala	Ala	Asp	
				380					385					390	



Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	
				185					190					195	
Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	
				200					205					210	
Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	
				215					220					225	
His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	
				230					235					240	
Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Val	Lys	Phe	Ser	Glu	Leu	
				245					250					255	
Leu	Trp	Gly	Gly	Lys	Gly	His	Arg	Arg	Leu	Phe	His	His	Ser	Leu	
				260					265					270	
Leu	Leu	Arg	Met	Ser	Ser	Leu	Leu	Ser	Asn	Ala	Leu	Leu	Pro	Ala	
				275					280					285	
Asp	Thr	Ser													
		288													

<210> 7  
 <211> 499  
 <212> PRT  
 <213> Unknown

<220>

<221> PEPTIDE  
 <223> Mouse Evi27 protein

<400> 7

Met	Leu	Leu	Val	Leu	Leu	Ile	Leu	Ala	Ala	Ser	Cys	Arg	Ser	Ala	
				5					10					15	
Leu	Pro	Arg	Glu	Pro	Thr	Ile	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	
				20					25					30	
Ser	Pro	Glu	Trp	Met	Val	Gln	His	Thr	Leu	Thr	Pro	Gly	Asp	Leu	
				35					40					45	
Arg	Asp	Leu	Gln	Val	Glu	Leu	Val	Lys	Thr	Ser	Val	Ala	Ala	Glu	
				50					55					60	
Glu	Phe	Ser	Ile	Leu	Met	Asn	Ile	Ser	Trp	Ile	Leu	Arg	Ala	Asp	
				65					70					75	
Ala	Ser	Ile	Arg	Leu	Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Ser	Gly	
				80					85					90	
Lys	Asn	Asn	Met	Asn	Ser	Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	
				95					100					105	
Glu	Ala	Phe	Gln	Ser	Gln	Thr	Arg	Pro	Ser	Gly	Gly	Lys	Trp	Thr	
				110					115					120	
Phe	Ser	Tyr	Val	Gly	Phe	Pro	Val	Glu	Leu	Ser	Thr	Leu	Tyr	Leu	
				125					130					135	
Ile	Ser	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Ser	
				140					145					150	
Pro	Ser	Leu	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asn	His	
				155					160					165	
Val	Met	Lys	Tyr	Lys	Lys	Gln	Cys	Thr	Glu	Ala	Gly	Ser	Leu	Trp	
				170					175					180	



Asp	Pro	Asp	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Lys	Met	Val	Glu
				185					190					195
Val	Asn	Phe	Thr	Thr	Asn	Pro	Leu	Gly	Asn	Arg	Tyr	Thr	Ile	Leu
				200					205					210
Ile	Gln	Arg	Asp	Thr	Thr	Leu	Gly	Phe	Ser	Arg	Val	Leu	Glu	Asn
				215					220					225
Lys	Leu	Met	Arg	Thr	Ser	Val	Ala	Ile	Pro	Val	Thr	Glu	Glu	Ser
				230					235					240
Glu	Gly	Ala	Val	Val	Gln	Leu	Thr	Pro	Tyr	Leu	His	Thr	Cys	Gly
				245					250					255
Asn	Asp	Cys	Ile	Arg	Arg	Glu	Gly	Thr	Val	Val	Leu	Cys	Ser	Glu
				260					265					270
Thr	Ser	Ala	Pro	Ile	Pro	Pro	Asp	Asp	Asn	Arg	Arg	Met	Leu	Gly
				275					280					285
Gly	Trp	Leu	Pro	Leu	Phe	Leu	Val	Leu	Leu	Val	Ala	Val	Trp	Val
				290					295					300
Leu	Ala	Ala	Gly	Ile	Tyr	Leu	Thr	Trp	Arg	Gln	Gly	Arg	Ser	Thr
				305					310					315
Lys	Thr	Ser	Phe	Pro	Ile	Ser	Thr	Met	Leu	Leu	Pro	Leu	Ile	Lys
				320					325					330
Val	Leu	Val	Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His	His	Thr	Val
				335					340					345
Cys	Arg	Phe	Thr	Asp	Phe	Leu	Gln	Asn	Tyr	Cys	Arg	Ser	Glu	Val
				350					355					360
Ile	Leu	Glu	Lys	Trp	Gln	Lys	Lys	Lys	Ile	Ala	Glu	Met	Gly	Pro
				365					370					375
Val	Gln	Trp	Leu	Thr	Thr	Gln	Lys	Gln	Ala	Ala	Asp	Lys	Val	Val
				380					385					390
Phe	Leu	Leu	Pro	Ser	Asp	Val	Pro	Thr	Leu	Cys	Asp	Ser	Ala	Cys
				395					400					405
Gly	His	Asn	Glu	Gly	Ser	Ala	Arg	Glu	Asn	Ser	Gln	Asp	Leu	Phe
				410					415					420
Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	Asp	Phe	Ser	Ser	Gln	Thr
				425					430					435
His	Leu	His	Lys	Tyr	Leu	Val	Val	Tyr	Leu	Gly	Gly	Ala	Asp	Leu
				440					445					450
Lys	Gly	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro	Gln	Tyr	His	Leu
				455					460					465
Met	Lys	Asp	Ala	Thr	Ala	Phe	His	Thr	Glu	Leu	Leu	Lys	Ala	Thr
				470					475					480
Gln	Ser	Met	Ser	Val	Lys	Lys	Arg	Ser	Gln	Ala	Cys	His	Asp	Ser
				485					490					495
Cys	Ser	Pro	Leu											
				499										

<210> 8  
 <211> 289  
 <212> PRT  
 <213> Unknown  
  
 <220>

[illegible]

<210>	9
<211>	866
<212>	PRT
<213>	Unknown
<220>	

<221> PEPTIDE  
 <223> IL-17 receptor protein

<400> 9

Met	Gly	Ala	Ala	Arg	Ser	Pro	Pro	Ser	Ala	Val	Pro	Gly	Pro	Leu	5	10	15
Leu	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Val	Leu	Ala	Pro	Gly	Gly	20	25	30
Ala	Ser	Leu	Arg	Leu	Leu	Asp	His	Arg	Ala	Leu	Val	Cys	Ser	Gln	35	40	45
Pro	Gly	Leu	Asn	Cys	Thr	Val	Lys	Asn	Ser	Thr	Cys	Leu	Asp	Asp	50	55	60
Ser	Trp	Ile	His	Pro	Arg	Asn	Leu	Thr	Pro	Ser	Ser	Pro	Lys	Asp	65	70	75
Leu	Gln	Ile	Gln	Leu	His	Phe	Ala	His	Thr	Gln	Gln	Gly	Asp	Leu	80	85	90
Phe	Pro	Val	Ala	His	Ile	Glu	Trp	Thr	Leu	Gln	Thr	Asp	Ala	Ser	95	100	105
Ile	Leu	Tyr	Leu	Glu	Gly	Ala	Glu	Leu	Ser	Val	Leu	Gln	Leu	Asn	110	115	120
Thr	Asn	Glu	Arg	Leu	Cys	Val	Arg	Phe	Glu	Phe	Leu	Ser	Lys	Leu	125	130	135
Arg	His	His	His	Arg	Arg	Trp	Arg	Phe	Thr	Phe	Ser	His	Phe	Val	140	145	150
Val	Asp	Pro	Asp	Gln	Glu	Tyr	Glu	Val	Thr	Val	His	His	Leu	Pro	155	160	165
Lys	Pro	Ile	Pro	Asp	Gly	Asp	Pro	Asn	His	Gln	Ser	Lys	Asn	Phe	170	175	180
Leu	Val	Pro	Asp	Cys	Glu	His	Ala	Arg	Met	Lys	Val	Thr	Thr	Pro	185	190	195
Cys	Met	Ser	Ser	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Val	Glu	200	205	210
Thr	Leu	Glu	Ala	His	Gln	Leu	Arg	Val	Ser	Phe	Thr	Leu	Trp	Asn	215	220	225
Glu	Ser	Thr	His	Tyr	Gln	Ile	Leu	Leu	Thr	Ser	Phe	Pro	His	Met	230	235	240
Glu	Asn	His	Ser	Cys	Phe	Glu	His	Met	His	His	Ile	Pro	Ala	Pro	245	250	255
Arg	Pro	Glu	Glu	Phe	His	Gln	Arg	Ser	Asn	Val	Thr	Leu	Thr	Leu	260	265	270
Arg	Asn	Leu	Lys	Gly	Cys	Cys	Arg	His	Gln	Val	Gln	Ile	Gln	Pro	275	280	285
Phe	Phe	Ser	Ser	Cys	Leu	Asn	Asp	Cys	Leu	Arg	His	Ser	Ala	Thr	290	295	300
Val	Ser	Cys	Pro	Glu	Met	Pro	Asp	Thr	Pro	Glu	Pro	Ile	Pro	Asp	305	310	315
Tyr	Met	Pro	Leu	Trp	Val	Tyr	Trp	Phe	Ile	Thr	Gly	Ile	Ser	Ile	320	325	330
Leu	Leu	Val	Gly	Ser	Val	Ile	Leu	Leu	Ile	Val	Cys	Met	Thr	Trp	335	340	345
Arg	Leu	Ala	Gly	Pro	Gly	Ser	Glu	Lys	Tyr	Ser	Asp	Asp	Thr	Lys	350	355	360

Tyr	Thr	Asp	Gly	Leu	Pro	Ala	Ala	Asp	Leu	Ile	Pro	Pro	Pro	Leu	365	370	375
Lys	Pro	Arg	Lys	Val	Trp	Ile	Ile	Tyr	Ser	Ala	Asp	His	Pro	Leu	380	385	390
Tyr	Val	Asp	Val	Val	Leu	Lys	Phe	Ala	Gln	Phe	Leu	Leu	Thr	Ala	395	400	405
Cys	Gly	Thr	Glu	Val	Ala	Leu	Asp	Leu	Leu	Glu	Glu	Gln	Ala	Ile	410	415	420
Ser	Glu	Ala	Gly	Val	Met	Thr	Trp	Val	Gly	Arg	Gln	Lys	Gln	Glu	425	430	435
Met	Val	Glu	Ser	Asn	Ser	Lys	Ile	Ile	Val	Leu	Cys	Ser	Arg	Gly	440	445	450
Thr	Arg	Ala	Lys	Trp	Gln	Ala	Leu	Leu	Gly	Arg	Gly	Ala	Pro	Val	455	460	465
Arg	Leu	Arg	Cys	Asp	His	Gly	Lys	Pro	Val	Gly	Asp	Leu	Phe	Thr	470	475	480
Ala	Ala	Met	Asn	Met	Ile	Leu	Pro	Asp	Phe	Lys	Arg	Pro	Ala	Cys	485	490	495
Phe	Gly	Thr	Tyr	Val	Val	Cys	Tyr	Phe	Ser	Glu	Val	Ser	Cys	Asp	500	505	510
Gly	Asp	Val	Pro	Asp	Leu	Phe	Gly	Ala	Ala	Pro	Arg	Tyr	Pro	Leu	515	520	525
Met	Asp	Arg	Phe	Glu	Glu	Val	Tyr	Phe	Arg	Ile	Gln	Asp	Leu	Glu	530	535	540
Met	Phe	Gln	Pro	Gly	Arg	Met	His	Arg	Val	Gly	Glu	Leu	Ser	Gly	545	550	555
Asp	Asn	Tyr	Leu	Arg	Ser	Pro	Gly	Gly	Arg	Gln	Leu	Arg	Ala	Ala	560	565	570
Leu	Asp	Arg	Phe	Arg	Asp	Trp	Gln	Val	Arg	Cys	Pro	Asp	Trp	Phe	575	580	585
Glu	Cys	Glu	Asn	Leu	Tyr	Ser	Ala	Asp	Asp	Gln	Asp	Ala	Pro	Ser	590	595	600
Leu	Asp	Glu	Glu	Val	Phe	Glu	Glu	Pro	Leu	Leu	Pro	Pro	Gly	Thr	605	610	615
Gly	Ile	Val	Lys	Arg	Ala	Pro	Leu	Val	Arg	Glu	Pro	Gly	Ser	Gln	620	625	630
Ala	Cys	Leu	Ala	Ile	Asp	Pro	Leu	Val	Gly	Glu	Glu	Gly	Gly	Ala	635	640	645
Ala	Val	Ala	Lys	Leu	Glu	Pro	His	Leu	Gln	Pro	Arg	Gly	Gln	Pro	650	655	660
Ala	Pro	Gln	Pro	Leu	His	Thr	Leu	Val	Leu	Ala	Ala	Glu	Glu	Gly	665	670	675
Ala	Leu	Val	Ala	Ala	Val	Glu	Pro	Gly	Pro	Leu	Ala	Asp	Gly	Ala	680	685	690
Ala	Val	Arg	Leu	Ala	Leu	Ala	Gly	Glu	Gly	Glu	Ala	Cys	Pro	Leu	695	700	705
Leu	Gly	Ser	Pro	Gly	Ala	Gly	Arg	Asn	Ser	Val	Leu	Phe	Leu	Pro	710	715	720
Val	Asp	Pro	Glu	Asp	Ser	Pro	Leu	Gly	Ser	Ser	Thr	Pro	Met	Ala	725	730	735
Ser	Pro	Asp	Leu	Leu	Pro	Glu	Asp	Val	Arg	Glu	His	Leu	Glu	Gly	740	745	750

Leu	Met	Leu	Ser	Leu	Phe	Glu	Gln	Ser	Leu	Ser	Cys	Gln	Ala	Gln
				755					760					765
Gly	Gly	Cys	Ser	Arg	Pro	Ala	Met	Val	Leu	Thr	Asp	Pro	His	Thr
				770					775					780
Pro	Tyr	Glu	Glu	Glu	Gln	Arg	Gln	Ser	Val	Gln	Ser	Asp	Gln	Gly
				785					790					795
Tyr	Ile	Ser	Arg	Ser	Ser	Pro	Gln	Pro	Pro	Glu	Gly	Leu	Thr	Glu
				800					805					810
Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Asp	Pro	Gly	Lys	Pro	Ala
				815					820					825
Leu	Pro	Leu	Ser	Pro	Glu	Asp	Leu	Glu	Ser	Leu	Pro	Ser	Leu	Gln
				830					835					840
Arg	Gln	Leu	Leu	Phe	Arg	Gln	Leu	Gln	Lys	Asn	Ser	Gly	Trp	Asp
				845					850					855
Thr	Met	Gly	Ser	Glu	Ser	Glu	Gly	Pro	Ser	Ala				
				860					865					

0976971.00001